

LOCUS AF089816 1765 bp mRNA linear PRI 24-OCT-1998
 DEFINITION Homo sapiens RGS-GAIP interacting protein GIPC mRNA, complete cds.
 ACCESSION AF089816
 VERSION AF089816.1 GI:3789933
 KEYWORDS .
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 1765)
 AUTHORS De Vries,L., Lou,X., Zhao,G., Zheng,B. and Farquhar,M.G.
 TITLE GIPC, a PDZ domain containing protein, interacts specifically with
 the C terminus of RGS-GAIP
 JOURNAL Proc. Natl. Acad. Sci. U.S.A. 95 (21), 12340-12345 (1998)
 MEDLINE 98445373
 PUBMED 9770488
 REFERENCE 2 (bases 1 to 1765)
 AUTHORS De Vries,L., Lou,X., Zhao,G., Zheng,B. and Farquhar,M.G.
 TITLE Direct Submission
 JOURNAL Submitted (03-SEP-1998) CMM, UCSD, 9500 Gilman Drive, La Jolla, CA
 92093, USA
 FEATURES Location/Qualifiers
 source 1..1765
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /cell_line="GC"
 /tissue_type="pituitary"
 /note="growth hormone secreting cells"
 CDS 88..1089
 /codon_start=1
 /product="RGS-GAIP interacting protein GIPC"
 /protein_id="AAC67548.1"
 /db_xref="GI:3789934"
 /translation="MPLGLGRRKKAPPLVENEAEPRGGGLGVGEPGPLGGGGSGGPQ
 MGLPPPPPALRPRLVFHTQLAHGSPTGRIEGFTNVKELYGKIAEAFRLPTAEVMFCTL
 NTHKVDMDKLLGGQIGLEDFIFAHVKGQRKEVEVFKSEDALGLTITDNGAGYAFIKRI
 KEGSVIDHIHLISVGDMEIAINGQSLGCRHYEVARLLKELPRGRTFTLKLTEPRKAF
 DMISQRSAGGRPGSGPQLGTGRGTLRLRSRGPATVEDLPSAFEKAIEKVDDLLESYM
 GIRDTELAATMVELGDKRNPDELAELDERLGDFAFPDEFVFDVWGAIGDAKVGRY"
 misc_feature 460..762
 /note="encodes PDZ domain"
 misc_feature 877..1047
 /note="encodes ACP domain"
 BASE COUNT 332 a 561 c 568 g 304 t
 ORIGIN

Alignment Scores:

Pred. No.:	2.08e-102	Length:	1765
Score:	1713.00	Matches:	330
Percent Similarity:	99.10%	Conservative:	0
Best Local Similarity:	99.10%	Mismatches:	3
Query Match:	99.59%	Indels:	0
DB:	9	Gaps:	0

US-10-013-056-2 (1-333) x AF089816 (1-1765)

Qy	1	MetProLeuGlyLeuGlyArgArgLysLysAlaProProLeuValGluAsnGluGluAla	20
Db	88	ATGCCGCTGGGACTGGGGCGCCGAAAAAGGCGCCCCCTCTAGTGGAAATGAGGAGGCT	147
Qy	21	GluProGlyArgGlyGlyLeuGlyValGlyGluProGlyProLeuGlyGlyGlySer	40
Db	148	GAGCCAGGCCGTGGAGGGCTGGGCGTGGGGGAGCCAGGGCCTTTGGGCGGAGGTGGGTTCG	207
Qy	41	Gly***ProGlnMetGly*****ProProProProAlaLeuArgProArgLeuValPhe	60
Db	208	GGGGGCCCCCAAATGGGCTTGCCCCCCCCCTCCCCAGCCCTGCGGCCCCGCTTGTGTTC	267
Qy	61	HisThrGlnLeuAlaHisGlySerProThrGlyArgIleGluGlyPheThrAsnValLys	80
Db	268	CACACCCAGCTGGCCCATGGCAGTCCCACTGGCCGCATCGAGGGGTTCACCAACGTCAAG	327
Qy	81	GluLeuTyrGlyLysIleAlaGluAlaPheArgLeuProThrAlaGluValMetPheCys	100
Db	328	GAGCTGTATGGCAAGATTGCCGAGGCCTTCCGCCTGCCAACTGCCGAGGTGATGTTTTGC	387
Qy	101	ThrLeuAsnThrHisLysValAspMetAspLysLeuLeuGlyGlyGlnIleGlyLeuGlu	120
Db	388	ACCTGAACACCCACAAAGTGGACATGGACAAGCTCCTGGGGGGCCAAATCGGGCTGGAG	447
Qy	121	AspPheIlePheAlaHisValLysGlyGlnArgLysGluValGluValPheLysSerGlu	140
Db	448	GACTTCATCTTCGCCCCAGTGAAGGGGCAGCGCAAGGAGGTGGAGGTGTTCAAGTCGGAG	507
Qy	141	AspAlaLeuGlyLeuThrIleThrAspAsnGlyAlaGlyTyrAlaPheIleLysArgIle	160
Db	508	GATGCACTCGGGCTCACCATCACGGACAACGGGGCTGGCTACGCCTTCATCAAGCGCATC	567
Qy	161	LysGluGlySerValIleAspHisIleHisLeuIleSerValGlyAspMetIleGluAla	180
Db	568	AAGGAGGGCAGCGTGATCGACCACATCCACCTCATCAGCGTGGGCGACATGATCGAGGCC	627
Qy	181	IleAsnGlyGlnSerLeuLeuGlyCysArgHisTyrGluValAlaArgLeuLeuLysGlu	200
Db	628	ATTAACGGGCAGAGCCTGCTGGGCTGCCGGCACTACGAAGTGGCCCGGCTGCTCAAGGAA	687
Qy	201	LeuProArgGlyArgThrPheThrLeuLysLeuThrGluProArgLysAlaPheAspMet	220
Db	688	CTGCCCCGAGGCCGTACCTTCACGCTGAAGCTCACGGAGCCTCGCAAGGCCTTCGACATG	747
Qy	221	IleSerGlnArgSerAlaGlyGlyArgProGlySerGlyProGlnLeuGlyThrGlyArg	240
Db	748	ATCAGCCAGCGTTTACGCGGTGGCCGCCCTGGCTCTGGCCCACTGGGCACTGGCCGA	807
Qy	241	GlyThrLeuArgLeuArgSerArgGlyProAlaThrValGluAspLeuProSerAlaPhe	260
Db	808	GGGACCCTGCGGCTCCGATCCCGGGGCCCCGCCACGGTGGAGGATCTGCCCTCTGCCTTT	867
Qy	261	GluGluLysAlaIleGluLysValAspAspLeuLeuGluSerTyrMetGlyIleArgAsp	280
Db	868	GAAGAGAAGGCCATTGAGAAGGTGGATGACCTGCTGGAGAGTTACATGGGTATCAGGGAC	927
Qy	281	ThrGluLeuAlaAlaThrMetValGluLeuGlyLysAspLysArgAsnProAspGluLeu	300

Db	928	ACGGAGCTGGCGGCCACCATGGTGGAGCTGGGAAAGGACAAAAGGAACCCGGATGAGCTG	987
Qy	301	AlaGluAlaLeuAspGluArgLeuGlyAspPheAlaPheProAspGluPheValPheAsp	320
Db	988	GCCGAGGCCCTGGACGAACGGCTGGGTGACTTTGCCTTCCCTGACGAGTTCGTCTTTGAC	1047
Qy	321	ValTrpGlyAlaIleGlyAspAlaLysValGlyArgTyr	333
Db	1048	GTCTGGGGCGCCATTGGGGACGCCAAGGTCGGCCGCTAC	1086